

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2002, 22:05:57 ; Search time 17398.4 seconds
(without alignments)
1042.620 Million cell updates/sec

Title: US-09-303-518D-127

Perfect score: 1344

Sequence: 1 atgattaaatcaaaaagg.....ccnttgagaaggaagctga 1344

Scoring table: IDENTITY.NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_estl:*

10: gb_est2:*

11: gb_hic:*

12: gb_gss:*

13: em_gss_hum:*

14: em_gss_inv:*

15: em_gss_pln:*

16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	108.6	8.1	349	12 CNS07GYI	AL610380 Anopheles
2	39.2	2.9	540	10 BF260729	BF260729 HVSMEF002
3	39.2	2.9	544	10 BF260723	BF260723 HVSMEF002
4	39.2	2.9	551	10 BF253989	BF253989 HVSMEF000
5	39.2	2.9	574	10 BF265938	BF265938 HV_Cea001
6	39.2	2.9	622	10 BF257371	BF257371 HVSMEF000
7	39.2	2.9	634	10 BF259896	BF259896 HVSMEF002
8	39.2	2.9	636	10 BF259473	BF259473 HVSMEF001
9	39.2	2.9	704	10 BF262832	BF262832 HVSMEF000
10	39.2	2.9	759	10 BF259476	BF259476 HVSMEF001
11	39.2	2.9	764	10 BF259476	BF259476 HVSMEF001
12	39.2	2.9	783	10 BF262832	BF262832 HVSMEF000
13	39.2	2.9	841	10 BF254527	BF254527 HVSMEF000
14	39.2	2.9	847	10 BF257008	BF257008 HVSMEF000
15	39.2	2.9	864	10 BF257786	BF257786 HVSMEF001
16	39.2	2.9	888	9 AW983120	AW983120 HVSMEF000
17	39	2.9	506	9 AI399239	AI399239 NCW10F2T3

18	39	2.9	621	10 BM490565	BM490565 ppg2n.pk0
19	38.2	2.8	455	10 BI956450	BI956450 HVSMEF000
20	37.6	2.8	489	9 AV939450	AV939450 AV939450
21	37.6	2.8	492	10 BE348841	BE348841 ht74905.x
22	37.6	2.8	575	10 BE551347	BE551347 hb33011.x
23	37.6	2.8	697	10 BF628426	BF628426 HVSMEF000
24	37.2	2.8	841	10 BG342965	BG342965 HVSMEF000
25	37	2.8	430	12 AZ049555	AZ049555 GSSBr0013
26	37	2.8	497	12 P9478	AL390645 Leishmani
27	36.8	2.7	893	9 AL523270	AL523270 AL523270
28	36.6	2.7	612	12 AQ161443	AQ161443 mgxb0007D
29	36.4	2.7	388	10 BM375129	BM375129 Ehem06_S0
30	36.2	2.7	682	9 AV917449	AV917449 AV917449
31	36	2.7	284	9 BE063171	BE063171 OV2-BF027
32	36	2.7	298	9 AA831113	AA831113 oc59a03.s
33	36	2.7	358	10 BF109446	BF109446 7152B06.x
34	36	2.7	384	9 AI392198	AI392198 NCSMD6T3
35	36	2.7	393	9 AI306569	AI306569 qn23e08.x
36	36	2.7	400	9 AI609778	AI609778 tf83b11.x
37	36	2.7	419	9 AA468664	AA468664 ne06c06.s
38	36	2.7	477	9 AI300364	AI300364 qn22e08.x
39	36	2.7	486	9 AI303130	AI303130 ox31a04.s
40	36	2.7	488	9 AI378387	AI378387 ct78e04.x
41	36	2.7	497	9 AI701002	AI701002 wt07f12.x
42	36	2.7	526	9 AW06812	AW06812 wt07f12.x
43	36	2.7	544	9 AI743812	AI743812 wq42b09.x
44	36	2.7	925	12 CNS0091P	AL053013 Drosophil
45	35.8	2.7	932	12 CNS01KFO	AL148277 Anopheles
46	35.6	2.7	1013	12 CNS04M5Y	AL297007 Tetraodon
47	35.6	2.6	413	9 AV631377	AV631377 AV631377
48	35.6	2.6	606	12 AQ160470	AQ160470 mgxb0005J
49	35.6	2.6	695	12 AQ162608	AQ162608 mgxb0013L
50	35.4	2.6	309	10 R23876	R23876 yH48g08.r1
51	35.4	2.6	421	10 BE423134	BE423134 WHE0061.F
52	35.4	2.6	479	10 BF233599	BF233599 WHE2158_G
53	35.4	2.6	526	10 BG262921	BG262921 WHE0948_G
54	35.4	2.6	561	10 BG262203	BG262203 WHE0873_B
55	35.4	2.6	580	10 BE430910	BE430910 SUN008.DO
56	35.4	2.6	599	10 BF483435	BF483435 WHE1794.H
57	35.4	2.6	617	12 AZ935303	AZ935303 BJ_Ba000
58	35.4	2.6	642	9 AA263267	AA263267 LD06355.5
59	35.4	2.6	702	10 BE414023	BE414023 SCU005.E0
60	35.4	2.6	704	10 BE413893	BE413893 SCU004.BO
61	35.4	2.6	849	10 BE642582	BE642582 Cr12_6.H0
62	35.2	2.6	613	10 BG577607	BG577607 Tm.ad.08D
63	35.2	2.6	642	9 AV273615	AV273615 AV273615
64	35.2	2.6	684	12 AZ085775	AZ085775 RPCI-23-2
65	35.2	2.6	797	10 BE412725	BE412725 MCG006.E0
66	35	2.6	356	10 H83299	H83299 ys89e09.sl
67	35	2.6	429	9 AI816996	AI816996 wj59c01.x
68	35	2.6	458	9 AW714071	AW714071 h5f02ne.f
69	35	2.6	620	10 BE425512	BE425512 WHE0317_B
70	35	2.6	802	9 AW48311	AW48311 BRV_541.B
71	35	2.6	826	10 BF624680	BF624680 HVSMEa001
72	35	2.6	892	10 BI836975	BI836975 603084506
73	34.8	2.6	275	9 AW574530	AW574530 UI-HF-BK0
74	34.8	2.6	488	9 AI452688	AI452688 tj56g03.x
75	34.6	2.6	323	9 AI368671	AI368671 qj61h02.x
76	34.6	2.6	376	10 BF233584	BF233584 WHE2158_E
77	34.6	2.6	407	9 AW712028	AW712028 f7c0lne.f
78	34.6	2.6	433	9 AW238848	AW238848 h29f02.y
79	34.6	2.6	497	10 BE378302	BE378302 601236326
80	34.6	2.6	501	10 BE396602	BE396602 601288849
81	34.6	2.6	525	10 BE407307	BE407307 601301064
82	34.6	2.6	554	10 BE792826	BE792826 601584823
83	34.6	2.6	582	10 BM042302	BM042302 603616381
84	34.6	2.6	605	10 BI195835	BI195835 602754956
85	34.6	2.6	605	10 BE907017	BE907017 601499836
86	34.6	2.6	609	12 FR004177	AL129269 Fugu rubr
87	34.6	2.6	624	10 BE394122	BE394122 601311607
88	34.6	2.6	627	10 BE302953	BE302953 ba71h10.y
89	34.6	2.6	636	10 BE255207	BE255207 601115757
90	34.6	2.6	659	10 BE254129	BE254129 601113992

91 34.6 2.6 671 10 BE794312
 92 34.6 2.6 676 10 BM042451
 93 34.6 2.6 683 10 BM006767
 94 34.6 2.6 686 10 BG761861
 95 34.6 2.6 691 10 BG469125
 96 34.6 2.6 721 10 BE299424
 97 34.6 2.6 727 10 BE612759
 98 34.6 2.6 733 10 BG165939
 99 34.6 2.6 762 10 B1161016
 100 34.6 2.6 764 10 BG481496

ALIGNMENTS

RESULT 1
 CENS07GYI 349 bp DNA linear GSS 02-OCT-2001
 LOCUS Anopheles gambiae GSS T7 end of clone 23L04 of library Notredame1
 DEFINITION from strain PEST of Anopheles gambiae (African malaria mosquito),
 genomic survey sequence.
 ACCESSION AL610380
 VERSION AL610380.1 GI:15916565
 KEYWORDS African malaria mosquito.
 SOURCE Anopheles gambiae
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
 Culicoidae; Anopheles.
 REFERENCE 1 (bases 1 to 349)
 Genoscope.
 AUTHORS Direct Submission
 TITLE Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 REFERENCE 2 (bases 1 to 349)
 Roth,C.W., Brey,P.T., Ke.Z. and Collins,F.H.
 AUTHORS Direct Submission
 TITLE Submitted (01-OCT-2001) BBMI, Institut Pasteur, 25, rue du Dr.
 JOURNAL Roux, Paris 75015, France
 COMMENT This clone is from an A. gambiae BAC library provided by F.H.
 Collins and sequenced by Genoscope in collaboration with the
 Laboratory of Biochem. and Biol. Molec. of Insects, Institut
 Pasteur.

FEATURES
 Source
 1. 349
 /organism="Anopheles gambiae"
 /strain="PEST"
 /db_xref="taxon:7165"
 /clone="23L04"
 /clone_lib="Notredame1"
 /note="end : T7"
 BASE COUNT 72 a 100 c 106 g 71 t
 ORIGIN
 Query Match 8.1%; Score 108.6; DB 12; Length 349;
 Best Local Similarity 59.0%; Pred. No. 1e-19;
 Matches 186; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
 Qy 629 atgaattggcgccgcgcattcggcgggttgagtcgacgacacattcattcattgagc 688
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 32 ATGAGTTTGTCTGCGCCGATCGCGGGGTCTGTGTCGGGAGCGACATCATCTTCCTTGCAG 91
 Qy 689 cggctcgtgcaaacacacgctttggaccattcaattcaagatgtaattgccatcgac 748
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 92 CGGTGAGCCTGACAAACAGCTCTGGCATCTTAATTATCAGGAGGTGATCGCCATCGGTA 151
 Qy 749 gttttgtgcaacagccgctctgaacacgagcgcttgattgctttgggtgggttctcaag 808
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 152 CGCTCTTCACATCGGAGAGCTGTGCGGGAACGCATCATCGCCATCGGTGGCGCCGAGG 211
 Qy 809 tcaaacacacgcctcttgcgtaccgcttttgggtgcgaagtagctgcaaatattactgcgg 868

Db 212 CTGCAAAACCGCGCTCTGGTGAAGACGCTGATTGGCGCGGATATCAATGAACCTGCTGAACG 271
 Qy 869 gcgaattggtgacgacgacacccggtgattccggttcggtattgaacgacgacgacgatta 928
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 272 AAGAAACCAAGACGACGCGCTGATTTCGGTTTCGGTCTCAGTGCCTGCATG 331
 Qy 929 cacaagggcgcgacg 943
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 332 CCGTGACGCGGCACG 346

RESULT 2
 BF260729 540 bp mRNA linear EST 22-OCT-2001
 LOCUS HVSMEF0022M15f Hordeum vulgare seedling root EST library HVCDNA0007
 DEFINITION (Etiolated and unstressed) Hordeum vulgare cdna clone
 HVSMEF0022M15f, mRNA sequence.
 ACCESSION BF260729
 VERSION BF260729
 KEYWORDS EST.
 SOURCE barley.
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 540)
 AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
 ,Y., Henry,D., Palmer,M., Rambo,J., Simmons,J., Choi,D.W., Fenton
 ,R.D., Oates,R. and Main,D.
 TITLE Development of a genetically and physically anchored EST resource
 JOURNAL for barley genomics: Morex unstressed seedling root cDNA library
 COMMENT Unpublished (2001)
 On Nov 16, 2000 this sequence version replaced gi:11189842.
 Contact: Wing RA

Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total hg bases = 241
 Seq primer: AATTAACCTCCTACTAAAGG
 High quality sequence stop: 530.
 FEATURES
 Location/Qualifiers
 1. 540
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSMEF0022M15f"
 /clone_lib="Hordeum vulgare seedling root EST library
 HVCDNA0007 (Etiolated and unstressed)"
 /tissue_type="Seedling root"
 /lab_host="TJCL21"
 /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
 Seeds were surface sterilized then germinated under axenic
 conditions in the dark at room temperature on filter paper
 with water, nystatin and cefotaxime in covered
 crystallization dishes. Five-day old seedling roots were
 then harvested, total RNA was prepared, poly(A) RNA was
 purified, one primary unamplified cDNA library was made,
 and 1 million pfu were in vivo excised to give pBluescript
 SK(-) cDNA phagemids. These steps were performed in the TJ
 Close laboratory at the University of California,
 Riverside (Choi, Close, Fenton). Phagemids were plated and
 picked at the Clemson University Genomics Institute (CUGI)
 (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
 preparations, DNA sequencing and sequence analysis were
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
 , Rambo, Main). The sequence has been trimmed to remove
 vector sequence and contains a minimum of 100 bases of
 phred value 20 or above. For more details on library
 preparation and sequence analysis see

<http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinof A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html>)"

BASE COUNT
ORIGIN

111 a 165 c 174 g 90 t

Query Match
Best Local Similarity 50.0%; Score 39.2; DB 10; Length 540;
Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 908 cggatattgaagcgcgacatacaagaagcgcacattattggagcctacacacac 967
DB 167 CGGTGATCTTCGACGCCGAGACGCGGACCGCTTCGACGTTCCGTTGACAAAGA 226
QY 968 agattccgttatcgaagaagcgcgacgaagcgtgttcggtgttcgacgcagc 1027
DB 227 AGATGGAGCTCTGCGACGTCGCGGACGACATGAGGTCTTCGCAAGGTGAGCGGGG 286
QY 1028 cggacaatactccatcacgcgttacgacctgagccattctctgaaacacaccttca 1087
DB 287 TGAGCTCTGACGCGGACGCGGACGCGGACGCGGACGCGGACGCGGACGCGG 346
QY 1088 agttcacgacagcgt 1103
DB 347 AGGCCAAGAGCGCCGT 362

RESULT 3
BF260723

LOCUS
DEFINITION
HVSMEF0022M09f Hordeum vulgare seedling root EST library HVCNMA0007 (Etiolated and unstressed) Hordeum vulgare cDNA clone
HVSMEF0022M09f, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BF260723 544 bp mRNA linear EST 22-OCT-2001
BF260723
EST.
barley.
Hordeum vulgare

REFERENCE
AUTHORS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.
1 (bases 1 to 544)
Wing, R., Close, T.J., Kleinof, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library

TITLE
JOURNAL
COMMENT

On Nov 16, 2000 this sequence version replaced gi:11189836.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: wing@clemson.edu
Total hg bases = 250
Seq primer: ATTACCTCTCACTAAGGG
High quality sequence stop: 512.
Location/Qualifiers

FEATURES
SOURCE

1..544
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEF0022M09f"
/clone_id="Hordeum vulgare seedling root EST library HVCNMA0007 (Etiolated and unstressed)"
/tissue_type="Seedling root"
/lab_host="TJC121"

BASE COUNT
ORIGIN

110 a 165 c 174 g 92 t

Query Match
Best Local Similarity 50.0%; Score 39.2; DB 10; Length 544;
Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 908 cggatattgaagcgcgacatacaagaagcgcacattattggagcctacacacac 967
DB 167 CGGTGATCTTCGACGCCGAGACGCGGACCGGACCGCTTCGACGTTCCGTTGACAAAGA 226
QY 968 agattccgttatcgaagaagcgcgacgaagcgtgttcggtgttcgacgcagc 1027
DB 227 AGATGGAGCTCTGCGACGTCGCGGACGACATGAGGTCTTCGCAAGGTGAGCGGGG 286
QY 1028 cggacaatactccatcacgcgttacgacctgagccattctctgaaacacaccttca 1087
DB 287 TGAGCTCTGACGCGGACGCGGACGCGGACGCGGACGCGGACGCGGACGCGG 346
QY 1088 agttcacgacagcgt 1103
DB 347 AGGCCAAGAGCGCCGT 362

RESULT 4
BF253989

LOCUS
DEFINITION
HVSMEF0022L01f Hordeum vulgare seedling root EST library HVCNMA0007 (Etiolated and unstressed) Hordeum vulgare cDNA clone
HVSMEF0022L01f, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BF253989 551 bp mRNA linear EST 22-OCT-2001
BF253989
EST.
barley.
Hordeum vulgare

REFERENCE
AUTHORS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.
1 (bases 1 to 551)
Wing, R., Close, T.J., Kleinof, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library

TITLE
JOURNAL
COMMENT

On Nov 16, 2000 this sequence version replaced gi:11183094.
Contact: Wing RA

/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and ceftaxime in covered crystallization dishes. Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million p10 were in vivo excised to give pluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinof A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html>)"

KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
1 (bases 1 to 704)
Wing, R., Close, T.J., Kleinbols, A., Wise, R., Begum, D., Frisch, D., Yu
, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
, R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex drought-stressed seedling shoot cDNA
library
Unpublished (2001)
On Dec 19, 2000 this sequence version replaced gi:11892790.
COMMENT Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 580
Seq primer: AATTAACCTCCTCAAGG
High quality sequence stop: 663.
FEATURES
Source
1..704
Location/Qualifiers
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSME0006N12f"
/clone_id="Hordeum vulgare seedling shoot EST library
HVCNMA0002 (Dehydration stress)"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and cefotaxime in covered
crystallization dishes. Five-day old seedlings were
incubated at 90% RH for 24 hr. Shoots were then harvested,
total RNA was prepared, poly(A) RNA was purified, one
primary unamplified cDNA library was made, 600000 pfu were
in vivo excised to give phagescript SK(-) cDNA phagemids.
These steps were performed in the TJ Close laboratory at
the University of California, Riverside (Choi, Close,
Fenton). Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinbols A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/gspages/bgn/31/cover.html)"

BASE COUNT

146 a 206 c 226 g 126 t

Query Match

Best Local Similarity 2.9%; Score 39.2; DB 10; Length 704;
Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 908 cggatcgaacgcgcgacatacacaagcgacgattatttgagcgtaccacaac 967
DB 164 CGGTGATCTTCACGCCGGAAGCACGGCGCGTCGACGCTTCGCTGACAAAGA 223

QY 968 agattccgtatcgaagaagccgcgacgaagcctcgttcgctggtgcgcgcagc 1027
DB 224 AGATGAGCTCTGTCGAGCTGCGACGACGACATCGAGGCTTCGCCAAGTGCAGCGCGGC 283
QY 1028 cggacaatactcctacgcgtacgacccctcgcgcacatcctcgaanaaactctca 1087
DB 284 TGACCTGCTGACCGCGGACGCGCGGAGAGGCCGCAAGTCATCACCCTCTGAGAGA 343
QY 1088 agttcagcaagccgt 1103
DB 344 AGGCCAAGAGCGCGCT 359
RESULT 10
BF259476
LOCUS
DEFINITION
HVSMEF0019D11f Hordeum vulgare seedling root EST library HVCNMA0007
HVSMEF0019D11f, mRNA sequence.
ACCESSION
BF259476
VERSION
BF259476
KEYWORDS
SOURCE
ORGANISM
Hordeum vulgare
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
1 (bases 1 to 759)
Wing, R., Close, T.J., Kleinbols, A., Wise, R., Begum, D., Frisch, D., Yu
, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
, R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex unstressed seedling root cDNA library
Unpublished (2001)
On Nov 16, 2000 this sequence version replaced gi:1188505.
COMMENT Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 469
Seq primer: AATTAACCTCCTCAAGG
High quality sequence stop: 663.
FEATURES
Source
1..759
Location/Qualifiers
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEF0019D11f"
/clone_id="Hordeum vulgare seedling root EST library
HVCNMA0007 (Etiolated and unstressed)"
/tissue_type="Seedling root"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and cefotaxime in covered
crystallization dishes. Five-day old seedling roots were
purified, total RNA was prepared, poly(A) RNA was
purified, one primary unamplified cDNA library was made,
and 1 million pfu were in vivo excised to give phagescript
SK(-) cDNA phagemids. These steps were performed in the TJ
Close laboratory at the University of California,
Riverside (Choi, Close, Fenton). Phagemids were plated and
picked at the Clemson University Genomics Institute (CUGI)
(Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
, Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library

preparation and sequence analysis see
<http://www.genome.clemson.edu/projects/barley>. To order
 this clone see <http://www.genome.clemson.edu/orders> Also
 see Close TJ, Wing R, Kleinof A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (<http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html>)

BASE COUNT 190 a 210 c 230 g 127 t
 ORIGIN

Query Match 2.9%; Score 39.2; DB 10; Length 759;
 Best Local Similarity 50.0%; Pred. No. 5.1;

Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 908 cggatggaacgagcgatgacaaagcgagcattttggagcctaccacaac 967
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 32 CGGTATCTTGACGCGGAGCAGCGGCGCGCTGCACGCTTCCGGTTGACAA 91
 Qy 968 agatttcgtatcgaagaagcgagcgaagagctgtgctgtgtgctgcgcagc 1027
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 92 AGATGAGAGCTGTGACGCTGCGGAGCAGATCGAGTCTTCCGCAAGTGAGCGGGG 151
 Qy 1028 cggacaatactcactacagcgtaacgacctgagcatttcctgaaacaactctca 1087
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 152 TGAGCTCGTACGCGGAGCGCGGAGCGCGCAATCATACACCCCTGCTGAGA 211
 Qy 1088 agttcagcagacgcgt 1103
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 212 AGGCCAAGAGCGCCGT 227

RESULT 11
 LOCUS BF616515 764 bp mRNA linear EST 22-OCT-2001
 DEFINITION HVSME0010E03f Hordeum vulgare seedling shoot EST library
 HVCNMA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone

ACCESSION BF616515
 VERSION BF616515.2 GI:13108021
 KEYWORDS EST.

SOURCE
 ORGANISM barley.
 Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Hordeum.
 1 (bases 1 to 764)

REFERENCE
 AUTHORS Wing R., Close T.J., Kleinof A., Wise R., Begum D., Frisch D., Yu
 T., Henry D., Palmer M., Rambo T., Simmons J., Choi D.W., Fenton
 R.D., Oates R. and Main D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex unstressed seedling shoot cDNA library
 Unpublished (2001)
 On Dec 18, 2000 this sequence version replaced gi:11880249.

JOURNAL
 COMMENT Contact: Wing RA
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: twing@clemson.edu
 Total hg bases = 395
 Seq primer: AATTACCCCTCCTCAAGG
 High quality sequence stop: 623.
 Location/Qualifiers

FEATURES
 source

1..764
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSME0010E03f"
 /clone_id="Hordeum vulgare seedling shoot EST library
 HVCNMA0003 (Etiolated and unstressed)"
 /tissue_type="Seedling shoot"

/lab_host="TJ0121"

/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
 Seeds were surface sterilized then germinated under axenic
 conditions in the dark at room temperature on filter paper
 with water, nystatin and cefotaxime in covered
 crystallization dishes. Five-day old seedling shoots were
 then harvested, total RNA was prepared, poly(A) RNA was
 purified, one primary unamplified cDNA library was made,
 and 1 million pin were in vivo excised to give pluescript
 SK(-) cDNA phagemids. These steps were performed in the TJ
 close laboratory at the University of California,
 Riverside (Choi, Close, Fenton). Phagemids were plated and
 picked at the Clemson University Genomics Institute (CUGI)
 (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
 preparations, DNA sequencing and sequence analysis were
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
 , Rambo, Main). The sequence has been trimmed to remove
 vector sequence and contains a minimum of 100 bases of
 phred value 20 or above. For more details on library
 preparation and sequence analysis see
<http://www.genome.clemson.edu/projects/barley>. To order
 this clone see <http://www.genome.clemson.edu/orders> Also
 see Close TJ, Wing R, Kleinof A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (<http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html>)"

BASE COUNT 177 a 217 c 243 g 127 t
 ORIGIN

Query Match 2.9%; Score 39.2; DB 10; Length 764;
 Best Local Similarity 50.0%; Pred. No. 5.1;

Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 908 cggatggaacgagcgatgacaaagcgagcattttggagcctaccacaac 967
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 167 CGGTATCTTGACGCGGAGCAGCGGCGCGCTGCACGCTTCCGGTTGACAA 226
 Qy 968 agatttcgtatcgaagaagcgagcgaagagctgtgctgtgtgctgcgcagc 1027
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 227 AGATGAGAGCTGTGACGCTGCGGAGCAGATCGAGTCTTCCGCAAGTGAGCGGGG 286
 Qy 1028 cggacaatactcactacagcgtaacgacctgagcatttcctgaaacaactctca 1087
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 287 TGAGCTCGTACGCGGAGCGCGGAGCGCGCAATCATACACCCCTGCTGAGA 346
 Qy 1088 agttcagcagacgcgt 1103
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 347 AGGCCAAGAGCGCCGT 362

RESULT 12
 LOCUS BF626740 783 bp mRNA linear EST 22-OCT-2001
 DEFINITION HVSME0010D17f Hordeum vulgare seedling shoot EST library
 HVCNMA0002 (Dehydration stress) Hordeum vulgare cDNA clone

ACCESSION BF626740
 VERSION BF626740.2 GI:13088174
 KEYWORDS EST.

SOURCE
 ORGANISM barley.
 Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Hordeum.
 1 (bases 1 to 783)

REFERENCE
 AUTHORS Wing R., Close T.J., Kleinof A., Wise R., Begum D., Frisch D., Yu
 T., Henry D., Palmer M., Rambo T., Simmons J., Choi D.W., Fenton
 R.D., Oates R. and Main D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex drought-stressed seedling shoot cDNA
 library
 Unpublished (2001)

JOURNAL
 Unpublished (2001)

Yr	Accession	Source	Organism	Title	Journal	Comment
908	cgatcttgaacggcggttacacaagaagcgagcaagctatattggaagcctaccacaatc					
968	agatttcggtatcaagaagaagcgcgcaagaagaagctgttcggcgtgggttcgcgcgaagc					
240	AGATGAGACCTCGTGTGACGTCGCGCAGCAGCATCGAGAGGTCTTCGCCAAAGGTGGAGCGCGGAC					
1028	cggacaatactcattcaacgcggttaagaccctcgagccattcttgaaacaacattca					
300	TGAGCTCTGTACGCCGCGAGCGCCGAGGAGCGCCCAAGTCATCATCACCTCTGTTGAGA					
1088	agttcagcagcagccgt	1103				
360	AGGCCAAGAGCGCCCT	375				
14	847 bp	22-OCT-2001				
1957008	B1957008	847 bp	mrna	linear	EST	22-OCT-2001
LOCUS	HVSMEN0006006f	Hordeum vulgare rachis EST library	HVCDNA0015			
DEFINITION	(normal) Hordeum vulgare cDNA clone HVSMEN0006006f, mRNA sequence.					
ACCESSION	B1957008					
VERSION	B1957008.1	GI:16308261				
KEYWORDS	EST.					
SOURCE	barley.					
ORGANISM	Hordeum vulgare					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae					
AUTHORS	Wing, R., Close, T.J., Kleinbols, A., Wise, R., Chin, A., Begum, D., Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R., and Main, D.					
TITLE	Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library.					
JOURNAL	Unpublished (2001)					
COMMENT	Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Total bp bases = 592 Seq primer: AATTAAACCTCTACTAAAGG High quality sequence stop: 667. Location/Qualifiers 1..847 /organism="Hordeum vulgare" /cultivar="Morex" /db_xref="taxon:4513" /clone="HVSMEN0006006f" /clone_11b="Hordeum vulgare rachis EST library HVCDNA0015 (normal)" /tissue_type="rachis" /lab_host="TJCl21" /note="vector: phluescript SK(-); Site.1: EcoRI; Site.2: XhoI; Plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinbols lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give phluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or					

```

/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSME0008022f"
/clone_1="Hordeum vulgare pre-anthesis spike EST library
HVCNAD0008 (white to yellow anther)"
/tissue_type="pre-anthesis spike"
/lab_host="SOLR"
/lambdazap="lambdazap, Site_1: Ecor1, Site_2: Xho1,
/notes="Vector: lambdazap, Site_1: Ecor1, Site_2: Xho1,

```

Query Match	2.98;	Score 39.2;	DB 9;	Length 888;
Best Local Similarity	50.08;	Pred. No. 5.5;		
Matches 98; Conservative	0;	Mismatches 98;	Indels 0;	Gaps 0

	QY	908	cggatattggaacgcgcgatataccaaagcgcgcaacgtattttggagcgtaccacaatc	967
	Db	166	CGGTGATCTTCAGACGCCGGAGACGGGCACGCCGCTGCAGCTCTTCCGGTTTCACACAGA	225
	QY	968	agatttcggtlatogaagaaggccgcgaacaaagaactgttctcgacttggttgcgcgcgacg	1027
	Db	226	AGATGAGACTCTCTCGACGTCGTGGCAGCAACATGAGAGCTTTCGCCAAGGTGGAGCGGGCG	285
	QY	1028	cggacaatatctcatcacagcgtltagacctctggscattctctgaaaaaacaaactcttca	1087
	Db	286	TGAAGCTGTAACGCCGGACGCCGCCAGAGAGCGCCGCAACTCATCACACCCTCTGTGAGA	345
	QY	1088	agttcacacgacagccgtt	1103
	Db	346	AGGCCAAAGACGCCGT	361
RESULT	17			
LOCUS	AI399239			
DEFINITION	NCM10F213 Westerngaards Neurospora crassa	506 bp	mRNA	linear
sequence.	sequence.			EST 08-FEB-1999
W10F2 5'				
CDNA clone				
w10f2				
mRNA				
Accession	AI399239			

JOURNAL
COMMENT

for barley genomics: Morex rachis cDNA library
Unpublished (2001)

Contact: Wing RA

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: twing@clemson.edu

Total hg bases = 327

Seq primer: AATTAACCCCTAAGGC

High quality sequence stop: 453.

FEATURES
source

Location/Qualifiers

1..453

/organism="Hordeum vulgare"

/cultivar="Morex"

/db_xref="taxon:4513"

/clone="HVSME0003623f"

/clone_lib="Hordeum vulgare rachis EST library HVCNDA0015 (normal)"

/tissue_type="rachis"

/lab_host="TJUC121"

/note="Vector: pBluescript SK(-); Site_1: EcoRI, Site_2: XhoI; plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinof's lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Fritsch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Fritsch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see

<http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinof's A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/g9pages/bgm/31/cover.html>)"

BASE COUNT 83 a 150 c 150 g 70 t 2 others

ORIGIN

Query Match 2.8%; Score 38.2; DB 10; Length 453;
Best Local Similarity 49.5%; Pred. No. 7.6;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 908 cggattgaagcgcgattacacaagcgcgacgattattggaagcaccacatc 967
DB 185 cggatgattcttcgacccggaaagcagcgacgacgcttcggttcgacagaga 244
QY 968 agatttcggtatcgaagaagcgcgacgaagcgttgcgtggttcgacgcagc 1027
DB 245 acatgagactctgctgacacgacgacgacgacgacgacgacgacgacgacgac 304
QY 1028 cggacaatactcactacgacgacgacgacgacgacgacgacgacgacgac 1087
DB 305 tgagctctgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 364
QY 1088 agttacagacagcgct 1103
DB 365 agcgcacagagcgccgt 380

RESULT 20
AV939450 489 bp mRNA linear EST 18-JAN-2002
LOCUS AV939450

DEFINITION

AV939450 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum

CDNA clone bdn22102 5', mRNA sequence.

AV939450.1 GI:18235247

EST.

Hordeum vulgare subsp. spontaneum.

Hordeum vulgare subsp. spontaneum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae

; Triticeae; Hordeum.

1 (bases 1 to 489)

Sato, K., Saitoh, D. and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadasu Shin-1

Center for Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshin@genes.nig.ac.jp.

Location/Qualifiers

1..489

/organism="Hordeum vulgare subsp. spontaneum"

/strain="H602"

/db_xref="taxon:77009"

/clone="bdn22102"

/clone_lib="K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves"

/tissue_type="top three leaves"

/dev_stage="adult, heading stage"

BASE COUNT 95 a 155 c 162 g 77 t

ORIGIN

Query Match 2.8%; Score 37.6; DB 9; Length 489;
Best Local Similarity 49.5%; Pred. No. 12;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 908 cggattgaagcgcgattacacaagcgcgacgattattggaagcaccacatc 967
DB 172 cggatgattcttcgacccggaaagcagcgacgacgacgacgacgacgacgacgac 231
QY 968 agatttcggtatcgaagaagcgcgacgaagcgttgcgtggttcgacgcagc 1027
DB 232 agatgagactctgctgacacgacgacgacgacgacgacgacgacgacgacgac 291
QY 1028 cggacaatactcactacgacgacgacgacgacgacgacgacgacgacgac 1087
DB 292 tgagctctgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 351
QY 1088 agttacagacagcgct 1103
DB 352 agcgcacagagcgccgt 367

RESULT 21
BE348841 492 bp mRNA linear EST 18-JUL-2000
LOCUS BE348841
DEFINITION ht74905.x1 NCI-GAP_Lu24 Homo sapiens cDNA clone IMAGE:3152504 3', similar to TR:013863 013863 HYPOTHETICAL 60.7 KD PROTEIN C1B1.02C IN CHROMOSOME 1.; contains element MERR22 repetitive element;; mRNA sequence.
ACCESSION BE348841
VERSION BE348841.1 GI:9260694
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 492)
NCI-GAP <http://www.ncbi.nlm.nih.gov/nclogap>.

High quality sequence stop: 681	FEATURES
Location/Qualifiers	source
1..697	

Db 129 CGCCGACGCGCCGAGGCGCCGACATCCATCCATCCCTGTGTGAGAGGCCAAGAG 188
QY 1098 agccgt 1103
Db 189 CGCGCT 194

RESULT 25
AZ049555/c 430 bp DNA linear GSS 06-MAR-2001
LOCUS GSSBrU01308 Sheared genomic library Brucella melitensis biovar
DEFINITION Abortus genomic clone M26, DNA sequence.
ACCESSION AZ049555
VERSION AZ049555.1 GI:7273470
KEYWORDS GSS.
SOURCE Brucella melitensis biovar Abortus.
ORGANISM Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
REFERENCE 1 (bases 1 to 430)
AUTHORS Sanchez,D.O., Zandomeni,R.O., Cravero,S., Verdun,R.E., Pierrou,E.,
Faccio,P., Diaz,G., Lanzavecchia,S., Aguero,F., Frisch,A.C.C.,
Andersson,S.G.E., Rosetti,O.L., Grau,O. and Ugalde,R.A.
Gene discovery through genomic sequencing of Brucella abortus
Infect. Immun. 69 (2), 865-868 (2001)
COMMENT Contact: Zandomeni, R.
Centro de Investigacion en Ciencias Agropecuarias (CICA)
Instituto Nacional de Tecnologia Agropecuaria (INTA) C.C. 25 (1712)
Castelar, Buenos Aires, Argentina
Tel: 5411-4621-3316/1683
Fax: 5411-4481-1316
Email: zandomeni@inta.gov.ar
Class: Shotgun.

FEATURES
source Location/Qualifiers
1..430
/organism="Brucella melitensis biovar Abortus"
/strain="S-2308"
/db_xref="taxon:235"
/clone="M26"
/note="Vector: pBluescript SK(-) (STRATAGENE); Genomic DNA
was mechanically sheared, blunt ended, and
size-fractionated by agarose gel electrophoresis.
Fragments between 1.5-3 kb were recovered and ligated to
the EcoRV site of the pBluescript SK (-) vector."

BASE COUNT 83 a 124 c 127 g 91 t 5 others
ORIGIN

Query Match 2.8%; Score 37; DB 12; Length 430;
Best Local Similarity 51.3%; Pred. No. 16;
Matches 79; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 442 gccatcttcgtcatgcatgacccaatccgctgngcagagccctgtgtgtatc 501
Db 221 GCCATGCTGCGCGATCCGCGCACGCGGAAGGTGGAGGAGATGATCGGC 162
QY 502 aaagaagccgngcngatgacagcngtctgctgcatgagccgttaccagcgt 561
Db 161 TTGATTCGCGCGCAATTTGAGTGAGCCCTTACAGCATGTTGCTTATAGCCGAGC 102
QY 562 aaatccatgtgttaaggcagctgagcagagc 595
Db 101 AATATCCGCAAGCAACGCACTGCGCACCGC 68

RESULT 26
P947R 497 bp DNA linear GSS 25-JUL-2000
LOCUS Leishmania major Friedlin PAC P947 right end-sequence, genomic
DEFINITION survey sequence.
ACCESSION AL390645
VERSION AL390645.1 GI:9501621

KEYWORDS GSS.
SOURCE Leishmania major.
ORGANISM Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania.
REFERENCE 1 (bases 1 to 497)
AUTHORS Ivens,A.C., Lewis,S.M., Bagherzadeh,A., Zhang,L., Chan,H.M. and
Smith,D.F.
TITLE A physical map of the Leishmania major Friedlin genome
JOURNAL Genome Res. 8 (2), 135-145 (1998)
MEDLINE 98146435
REFERENCE 2 (bases 1 to 497)
AUTHORS Taylor,R.G., Huckle,E.F.J., Ivens,A.C., Rejandream,M.A. and
Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (24-JUL-2000) Leishmania major Friedlin genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
alicates@sanger.ac.uk
see <http://www.edi.ac.uk/parasites/leish.html>
details of Leishmania sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/L_maj/
The primer sequence can be obtained from alicates@sanger.ac.uk.

COMMENT

FEATURES
source Location/Qualifiers
1..497
/organism="Leishmania major"
/strain="Friedlin"
/db_xref="taxon:5664"
/clone="PAC P947"

BASE COUNT 74 a 172 c 145 g 104 t 2 others
ORIGIN

Query Match 2.8%; Score 37; DB 12; Length 497;
Best Local Similarity 58.7%; Pred. No. 17;
Matches 64; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1172 ctacctgttgcgcgcatatcgtcgcgataccagcagcgcgcaagattgggt 1231
Db 231 CGACGCTGCTGGCGCACGGGCTGCGCGCGCCACCGTCCGCGCTAGCGCC 290
QY 1232 gcttgaattgaggaagaagacctcgttctgtgcagctctgcgc 1280
Db 291 GCCAGCAACAGACGACACCCCGCTGTGATGCTGATGCTGCTTCC 339

RESULT 27
AL523270 893 bp mRNA linear EST 13-FEB-2001
LOCUS AL523270 LTL_NFL003_NBC3 Homo sapiens cDNA clone CS0DC001YH12 5
DEFINITION prime, mRNA sequence.
ACCESSION AL523270
VERSION AL523270.1 GI:12786763
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 893)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segre@genoscope.cns.fr; Web : www.genoscope.cns.fr.

FEATURES
source Location/Qualifiers
1..893
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC001YH12"
/clone_lib="LTL_NFL003_NBC3"
/sex="male"


```

/organism="Magnaporthe grisea"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0007020"
/clone_lib="CGI Rice Blast BAC Library"
/issue_type="Protoplasts"
/lab_host="E. coli DH10s"
/notes="Vector: pBACWCH; Site 1: HindIII; Site 2: HindIII
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with

```

```

/organism="Hordeum vulgare"
/cultivar="Optic"
/db_xref="taxon:4513"
/clone="EBem06_S0002_H03"
/clone_lib="IGF Barley EBem06 library"
/tissue_type="Embryo"
/dev_stage="21 days post anthesis"

```


QY 608 atgtctgcaacatcgaaacatgaattcggtgcccgcgcgttcgttgatgca 667
|||||
Db 162 ATGCTACCACTCCCTCCATCTGTGTGCGGAGCCCGTGAAGCAGCTTGTGAGAGCCT 103
QY 668 cgcacatcattcatcattgagccggtcggtgcaaacacacggtttga 715
|||||
Db 102 CGCCCAAGTGCCTGCTGATTGGAAGCTCCGGAAGAAGCAAGCCACTTCA 55

RESULT 32
AA831113
LOCUS
DEFINITION
298 bp mRNA linear EST 07-APR-1998
cc59a03.s1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:135364.3
similar to SW:YER1_YEAST P32622 HYPOHETICAL 55.9 KD PROTEIN IN
GDA1-UTR2 INTERGENIC REGION; contains element TAR1 repetitive
element ; mRNA sequence.

ACCESSION
AA831113
VERSION
AA831113.1 GI:2904212
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 298)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/dbirp/image/image.html
Insert length: 830 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 277.

FEATURES
source
Location/Qualifiers
1..298
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:135364"
/clone_lib="NCI-CGAP_GCBI"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CIBR). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGCCGCTATTTTTTTTTTTT-3',
15'-TGTTACCAATCTGAAGTGGAGCGCGCCGCTATTTTTTTTTTTT-3',
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
69 a 84 c 93 g 52 t
ORIGIN

Query Match 2.7% Score 36; DB 9; Length 298;
Best Local Similarity 58.3%; Pred. No. 26;
Matches 63; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 608 atgtctgcaacatcgaaacatgaattcggtgcccgcgcgttcgttgatgca 667
|||||

Db 146 ATGCTACCACTCCCTCCATCTGTGTGCGGAGCCCGTGAAGCAGCTTGTGAGAGCCT 205
QY 668 cgcacatcattcatcattgagccggtcggtgcaaacacacggtttga 715
|||||
Db 206 CGCCCAAGTGCCTGCTGATTGGAAGCTCCGGAAGAAGCAAGCCACTTCA 253

RESULT 33
BF109446
LOCUS
DEFINITION
358 bp mRNA linear EST 20-OCT-2000
7152b06.x1 Soares NSF_F8_9W_OT_PA_P.S1 Homo sapiens cDNA clone
IMAGE:3525058.3 similar to TR:Q9V655 Q9V6R5 CG6152 PROTEIN. [1]
; contains element MER22 repetitive element ; mRNA sequence.

ACCESSION
BF109446
VERSION
BF109446.1 GI:10939136
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 358)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
Seq primer: -40UP from Glbco
High quality sequence stop: 329.

FEATURES
source
Location/Qualifiers
1..358
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3525058"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P.S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHSF pool 1:
309384-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002
150407, 151176-152327 Soares NB2HF8-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NBHOF
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT
77 a 114 c 109 g 58 t
ORIGIN

Query Match 2.7% Score 36; DB 10; Length 358;
Best Local Similarity 58.3%; Pred. No. 28;
Matches 63; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 608 atgtctgcaacatcgaaacatgaattcggtgcccgcgcgttcgttgatgca 667
|||||
Db 222 ATGCTACCACTCCCTCCATCTGTGTGCGGAGCCCGTGAAGCAGCTTGTGAGAGCCT 281
QY 668 cgcacatcattcatcattgagccggtcggtgcaaacacacggtttga 715
|||||
Db 282 CGCCCAAGTGCCTGCTGATTGGAAGCTCCGGAAGAAGCAAGCCACTTCA 329

RESULT 34
AI392198/c

Query Match 2.7%; Score 36; DB 9; Length 488;
Best Local Similarity 58.3%; Pred. No. 33;
Matches 63; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 608 atgtgcacacatgaacatgaattcgagcgccgcatcgccggtttgagtga 667
Db 222 ATGCTACCCGCTCCCTCCATCTGTGTGCGGAGACCCCGAGACGCGTGTGAGAGCCT 281

Qy 668 cgcacattcattcattgagccggtcggtgcaacaaacggtttga 715
Db 282 CGCCAGTGCCTGCATTGGAAGCTCCGGAAGAAGCAAGCCACTTGA 329

RESULT 41
AT701002 497 bp mRNA linear EST 18-DEC-1999
LOCUS we09e08.x1 NCI-CGAP Lu24 Homo sapiens cDNA clone IMAGE:2340614 3'
DEFINITION similar to TR:013863 013863 HYPOTHETICAL 60.7 KD PROTEIN C1B1.02C
IN CHROMOSOME 1.; contains element MER22 MER22 repetitive element
; mRNA sequence.

ACCESSION AT701002 GI:4988902
VERSION AT701002.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 497)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bdrrp/image/image.html
Insert Length: 760 Std Error: 0.00
Seq primer: -400p from Gibco
High quality sequence stop: 461.
Location/Qualifiers

FEATURES
source
1. .497
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2340614"
/clone_lib="NCI-CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: lung; Vector: pRT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI-CGAP_Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonoids
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo.

BASE COUNT 98 a 162 c 144 g 93 t
ORIGIN

Query Match 2.7%; Score 36; DB 9; Length 497;
Best Local Similarity 58.3%; Pred. No. 33;
Matches 63; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 608 atgtgcacacatgaacatgaattcgagcgccgcatcgccggtttgagtga 667
Db 222 ATGCTACCCGCTCCCTCCATCTGTGTGCGGAGACCCCGAGACGCGTGTGAGAGCCT 281

Qy 668 cgcacattcattcattgagccggtcggtgcaacaaacggtttga 715
Db 282 CGCCAGTGCCTGCATTGGAAGCTCCGGAAGAAGCAAGCCACTTGA 329

RESULT 42
AM006812 526 bp mRNA linear EST 10-SEP-1999
LOCUS w070712.x1 NCI-CGAP Co3 Homo sapiens cDNA clone IMAGE:2506799 3'
DEFINITION similar to TR:013863 013863 HYPOTHETICAL 60.7 KD PROTEIN C1B1.02C
IN CHROMOSOME 1.; contains element MER22 MER22 repetitive element
; mRNA sequence.

ACCESSION AM006812
VERSION AM006812.1 GI:5855590
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 526)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bdrrp/image/image.html
Seq primer: -400p from Gibco
High quality sequence stop: 470.
Location/Qualifiers

FEATURES
source
1. .526
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2506799"
/clone_lib="NCI-CGAP_Co3"
/sex="pooled"
/tissue_type="colon"
/lab_host="DH10B"
/note="Vector: pRT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from 12 pooled bulk tumor samples and primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pRT73 vector. Library went through one round of
normalization."

BASE COUNT 106 a 165 c 143 g 111 t 1 others
ORIGIN

Query Match 2.7%; Score 36; DB 9; Length 526;
Best Local Similarity 58.3%; Pred. No. 34;
Matches 63; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 608 atgtgcacacatgaacatgaattcgagcgccgcatcgccggtttgagtga 667
Db 204 ATGCTACCCGCTCCCTCCATCTGTGTGCGGAGACCCCGAGACGCGTGTGAGAGCCT 263

Qy 668 cgcacattcattcattgagccggtcggtgcaacaaacggtttga 715
Db 264 CGCCAGTGCCTGCATTGGAAGCTCCGGAAGAAGCAAGCCACTTGA 311

RESULT 43
AT743812

LOCUS	AI743812		544 bp	MRA	linear	EST 19-DEC-1998
DEFINITION	wg42db09.x1 Soares NSF_F8_9W_OT_PA.P.SI Homo sapiens cDNA clone IMAGE:2367737 3' similar to TR:O13863 O13863 HYPOHECTAL 60.7 KD PROTEIN C1B1.02C IN CHROMOSOME 1.; contains element MER22 repetitive element ; , mRNA sequence.					
ACCESSION	AI743812					
VERSION	AI743812.1		GI:5112100			
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	N1 (bases 1 to 544) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index					
JOURNAL	Unpublished (1997)					
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov This clone is available royalty-free through LNLN; contact the IMAGE Consortium (infoimage.lnl.nih.gov) for further information. Insert Length: 1033 Std Error: 0.00 Seq primer: -40UP from Glbpco High quality sequence stop: 496. Location/Qualifiers					
FEATURES	source					
	1..544					
	/organism="Homo sapiens"					
	/db_xref="taxon:9606"					
	/clone="IMAGE:2367737"					
	/clone_lib="Soares_NSF_F8_9W_OT_PA.P.S1"					
	/lab_host="DH10B"					
	/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clones: Soares NBHSF pool 1: 309984-310919, 323208-325895 Soares NB2HP pool 1: 145032-147335, 147720-148103, 148672-149255, 15002 - 150047, 151176-152327 Soares NB2HR-9W pool 1: 758280-760583, 772104-774407 Soares NBHF pool 1: 304776-306311, 320136-322823, 326280-326653 Soares NBHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bentic Soares and M. Fatima Bonaldo."					
BASE COUNT	106 a 173 c 154 g 111 t					
ORIGIN						
	Query Match 2.7%; Score 36; DB 9; Length 544; Best Local Similarity 58.3%; Pred. No. 34; Matches 63; Conservative 0; Mismatches 45; Indels 0; Gaps 0;					
QY	608 atgcggccaactcgaacaatgatattcgaggccgcagctcggccggttgagtga 667 					
Db	222 ATGTACTCCACATCCCCTTCATCTGTGTGGAGACCCTTGAGACGCTT 281 					
QY	668 cgcacatcatcttcattgaccggtcgtgycacaacaacgcttga 715 					
Db	282 CCCCAAGTGCCTGATTGGACGTCGCCGAAGAAGCACCTTCGA 329 					
RESULT 44						
CNS0091P/C	CNS0091P	925 bp	DNA	linear	GSS 03-JUN-1998	
DEFINITION	Drosophila melanogaster genome survey sequence TEJ3 end of BAC # BACH19P16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.					
ACCESSION	AI053013					
VERSION	AI053013.1		GI:4934461			
KEYWORDS	GSS.					

SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 925)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Web : www.genoscope.cns.fr)
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org/The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oseegawa and Aaron Mammosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPc1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the library pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. Location/Qualifiers 1..925 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone_lib="RPc1-98" /clone="BACR19D16" /note="end : TET3"
FEATURES	source
BASE COUNT	120 a 61 c 61 g 172 t 511 others
ORIGIN	
Query Match	2.7%; Score 36; DB 12; Length 925;
Best Local Similarity	11.9%; Pred. No. 44;
Matches	34; Conservative 128; Mismatches 124; Indels 0; Gaps 0.
Gy	388 ggcgcgtanccgcttcagcaaatcccctcgcttcgaagcgcagccgttcgcatc 447
Db	914 SSBGCGSSSMGTSSNSBSBSCSSBSSTYSMSNBSBSSSGSSSGTTSACVWC 855
Gy	448 ttgcgtaatgcgatggacaaccaatccgcttgcgcgcagaccctgtgttgatcaaga 507
Db	854 NASSSGCGCGCMACBCMCSSSCGSASAGVVRASGGAKRGKGGSGGASASHSSS 795
Gy	508 gccgcgngangatttaagcngantgtcgtgatatgcgcgtttaacgagcgttaaact 567
Db	794 ACBSSSSSCSACWSAASSSSASRSRNRGGAGGAGSGASSSSSSSASAGSVYSSAS 735
Gy	568 catgttgtlaaggacagtgcgcagacagtgcgcgttcgtgaanaatgtctgcacaactga 627
Db	734 SSSSSCSSSVSCSAVSSMCSBSSSSASASASSSSSSSSASCASCCTTSMSCSTSA 675
Gy	628 catgattcgcgcgccgcgcatccgcgcgttgattgaatggagcacaca 673
Db	674 SMSARSSSSSSSCSSSMSASASSASASSSSSSSSSSSSSSGGA 629
RESULT	45
CNSOLIC/KFO/C	932 bp DNA linear GSS 12-JUN-2001
LOCUS	Anopheles gambiae GSS 17 end of clone 16023 of NotreDame1 library
DEFINITION	from strain FEST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.
ACCESSION	AL148277
VERSION	ALI48277.1 GI:7006423
KEYWORDS	GSS.
SOURCE	African malaria mosquito.
ORGANISM	Anopheles gambiae

REFERENCE Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidae; Anopheles.

AUTHORS 1 (bases 1 to 932)
TITLE Genoscope.
JOURNAL Direct Submission

REFERENCE Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segreffgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
2 (bases 1 to 932)

AUTHORS Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-2000) BMJ, Institut Pasteur, 25, rue du Dr.
Roux, Paris 75015, France

COMMENT This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
Pasteur.

FEATURES Location/Qualifiers

1..932
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="16023"
/clone_lib="Notredame1"
/note="end : 17"

BASE COUNT 159 a 278 c 269 g 215 t 11 others
ORIGIN

Query Match 2.7%; Score 35.8; DB 12; Length 932;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 82; Conservative 1; Mismatches 81; Indels 0; Gaps 0;

OY 74 tcattaccgaagtcgctgttctggaagaatgacggtatgccccctngatgaag 133
DB 779 TGTATGAACCTGGCCGAGAGTTTGAAGTGTGATATGACGGCTGGGGAACCTACTTCGAAG 720
OY 134 tcaaggaaggcgatgccgtcaaaaaagccaagtgtgttgaagacaanaaagatccg 193
DB 719 ATCCGAACGGTGAAGACGGCGAAGAGGACGACGAGATTACGCTGACGAGAGCGACG 660
OY 194 gctgtgtgtttaccggtcgtcgttcaagcaaaatcgccgcac 237
DB 659 ACGGCGTGGTCACTAAGCGTTTTCAGGSGTGGCGCGCCACAC 616

Search completed: June 29, 2002, 22:06:22
Job time: 1755 sec

